



**P L A N T & A N I M A L G E N O M E X X I I I**

The Largest Ag-Genomics Meeting in the World.

January 10-14, 2015  
San Diego, CA

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- Browse by Type
- Author Index
- Poster Categories

Meeting Information

**When:** January 10 - 14, 2015  
**Where:** San Diego, CA

W448

Enabling Knowledge Management in the Agronomic Domain

Date: Wednesday, January 14, 2015  
Time: 10:50 AM  
Room: Pacific Salon 2

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The drastic growth in data in the recent years, within the Agronomic sciences has brought the concept of knowledge management to the forefront. Some of the factors that contribute to this change include a) conducting high-throughput experiments have become affordable, the time spent in generating data through these experiments are minuscule when compared to its integration and analysis; b) publishing data over the web is fairly trivial and c) multiple databases exist for each type of data (i.e. 'omics' data) with a possible overlap or slight variation in its coverage [1, 2]. In most cases these sources remain autonomous and disconnected. Hence, efficiently managed data and the underlying knowledge in principle will make data analysis straightforward aiding in more efficient decision making. At the Institute of Computational Biology (IBC), we are involved in developing methods to aid data integration and knowledge management within the domain of Agronomic sciences to improve information accessibility and interoperability. To this end, we address the challenge by pursuing several complementary research directions towards: distributed, heterogeneous data integration.

This talk will focus mainly on, ongoing projects at IBC:

- a) Agronomic Linked Data (AgroLD): is a Semantic Web knowledge base designed to integrate data from various publically available plant centric data sources. These include Gramene, Oryzabase, TAIR and resources from the South Green platform among many others. The aim of AgroLD project is to provide a portal for bioinformaticians and domain experts to exploit the homogenized data towards enabling to bridge the knowledge.
- b) GIGwA: is a tool developed to manage genomic, transcriptomic and genotyping large data resulting from NGS analyses. Often biologists are required to handle large VCF files to filter, query and extract data for their research. The existing tools are mainly targeted for experienced users by providing command line APIs. With GIGwA, we aim to provide a web user interface to make the system accessible to users from the biological field.

References:

Goble, C. and Stevens, R. (2008) State of the nation in data integration for bioinformatics. *Journal of Biomedical Informatics*, **41**(5), 687-693.

Antezana, E., et al. (2009) Biological knowledge management: the emerging role of the Semantic Web technologies. *Brief. in Bioinformatics*, **10**(4), 392-407.

Back to: [International Rice Informatics Consortium](#)

[<< Previous Abstract](#) | [Next Abstract >>](#)